

FIGURE 1

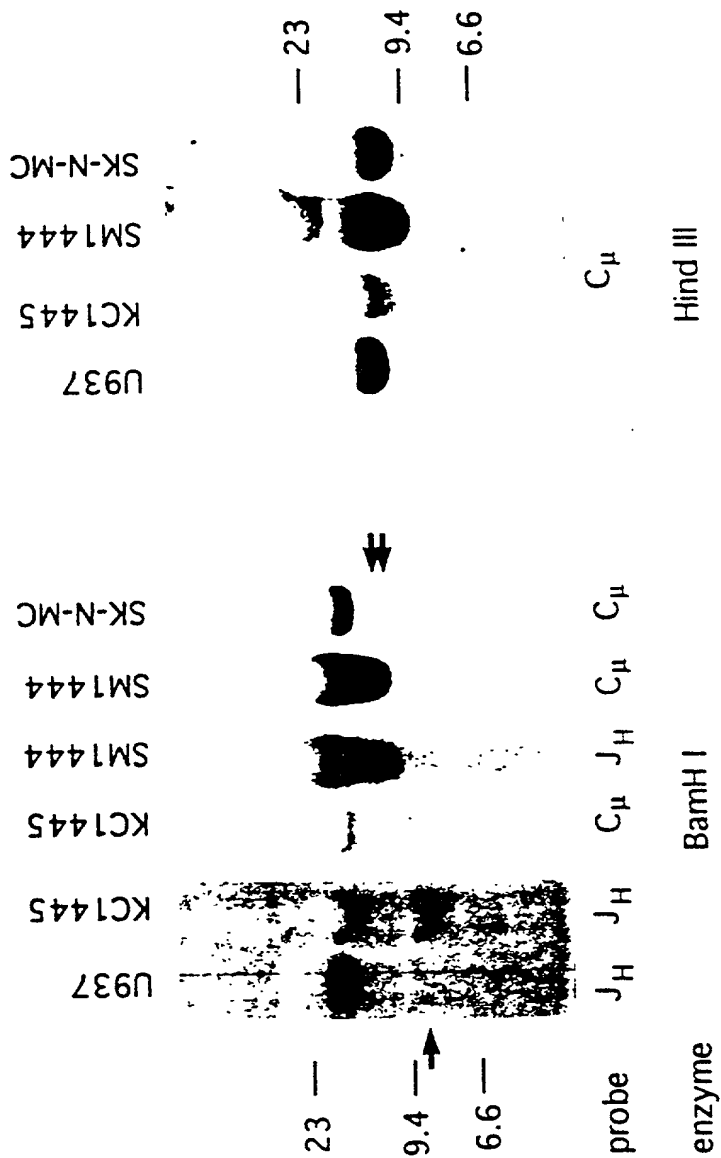
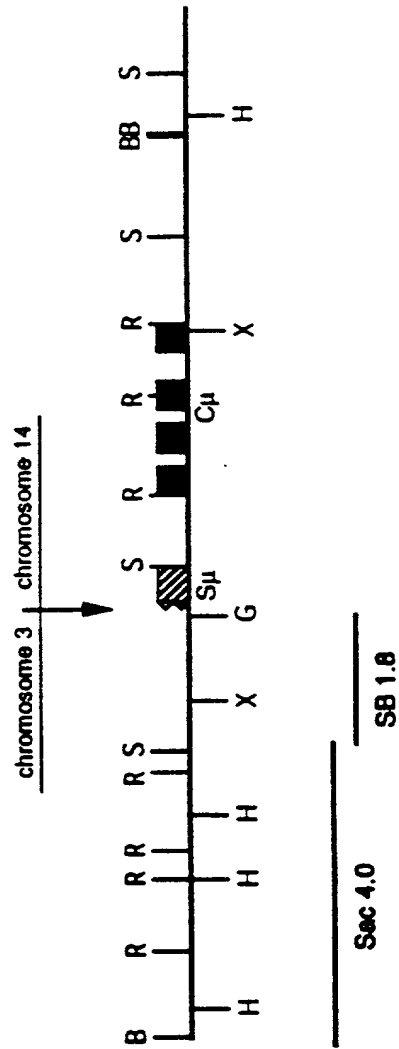
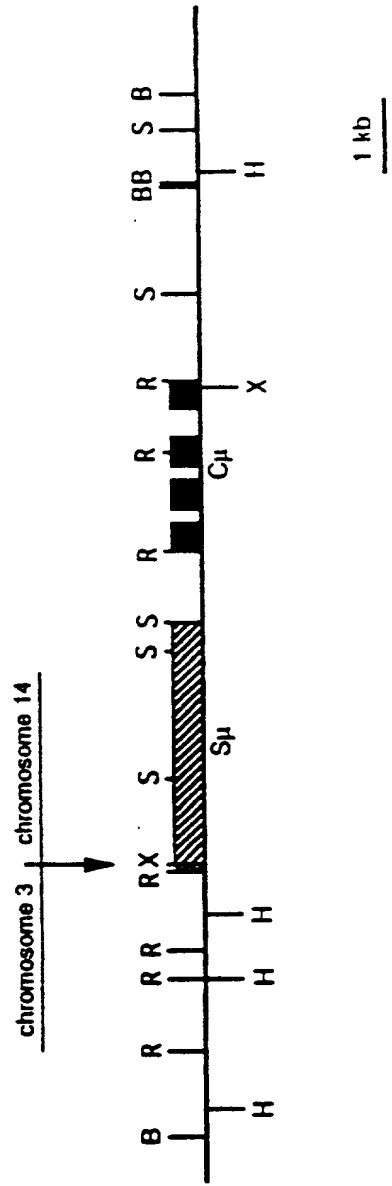


FIGURE 2

SM-71

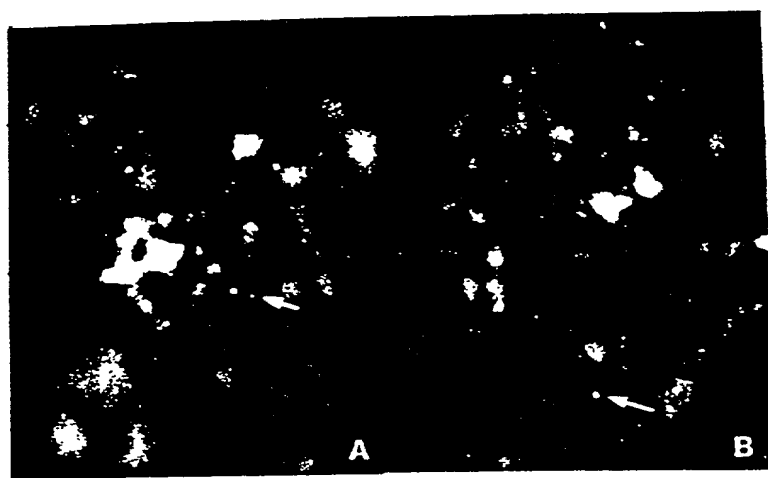


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FIGURE 3



**FIGURE 4A**

U937  
SM1444  
KC1445  
SK-N-MC

9.4 —  
6.6 —  
4.4 —  
2.3 —  
2.0 —  
1.4 —

enzyme  
EcoR I  
probe  
SB1.8

**FIGURE 4B**

U937  
TF1403  
LD1411  
SM1444  
KC1445  
SK-N-MC

2.3 —  
9.4 —  
6.6 —  
4.4 —

Bgl II  
Sac 4.0

**FIGURE 4C**

U937  
EM352  
CF755  
SO955  
SK-N-MC

2.3 —  
9.4 —  
6.6 —  
4.4 —  
2.3 —  
2.0 —  
1.4 —

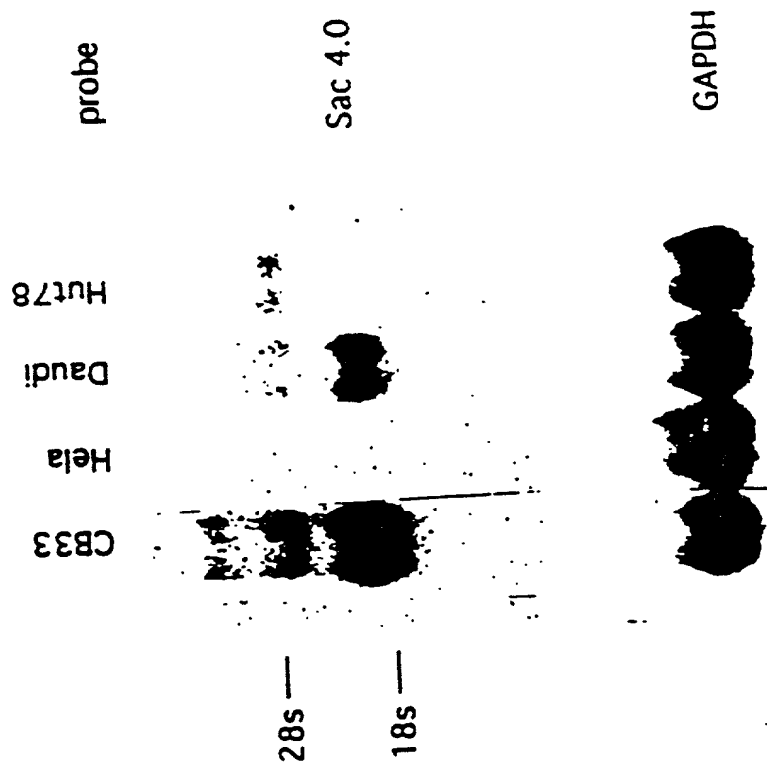
Bgl II  
Sac 4.0

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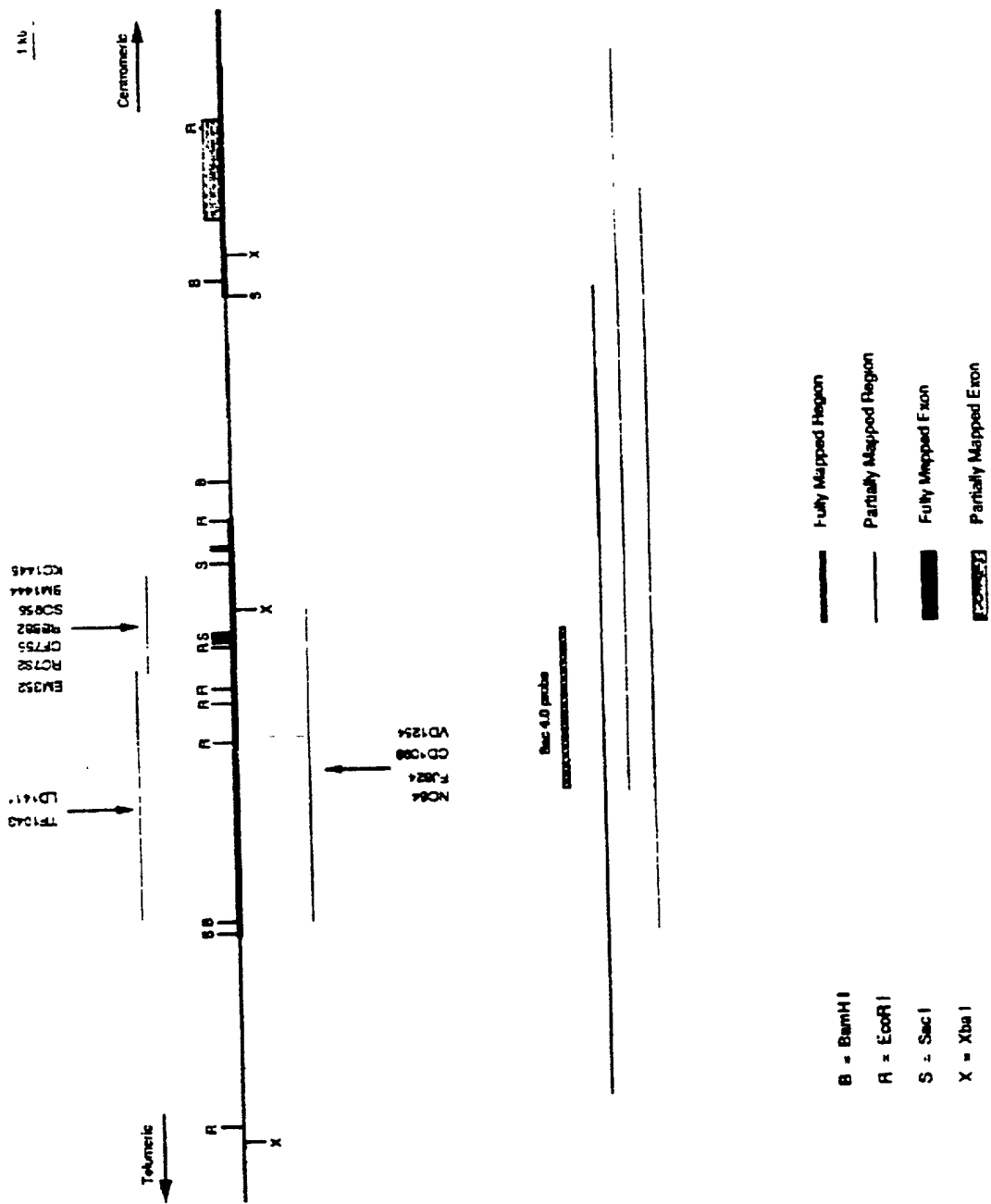
FIGURE 5



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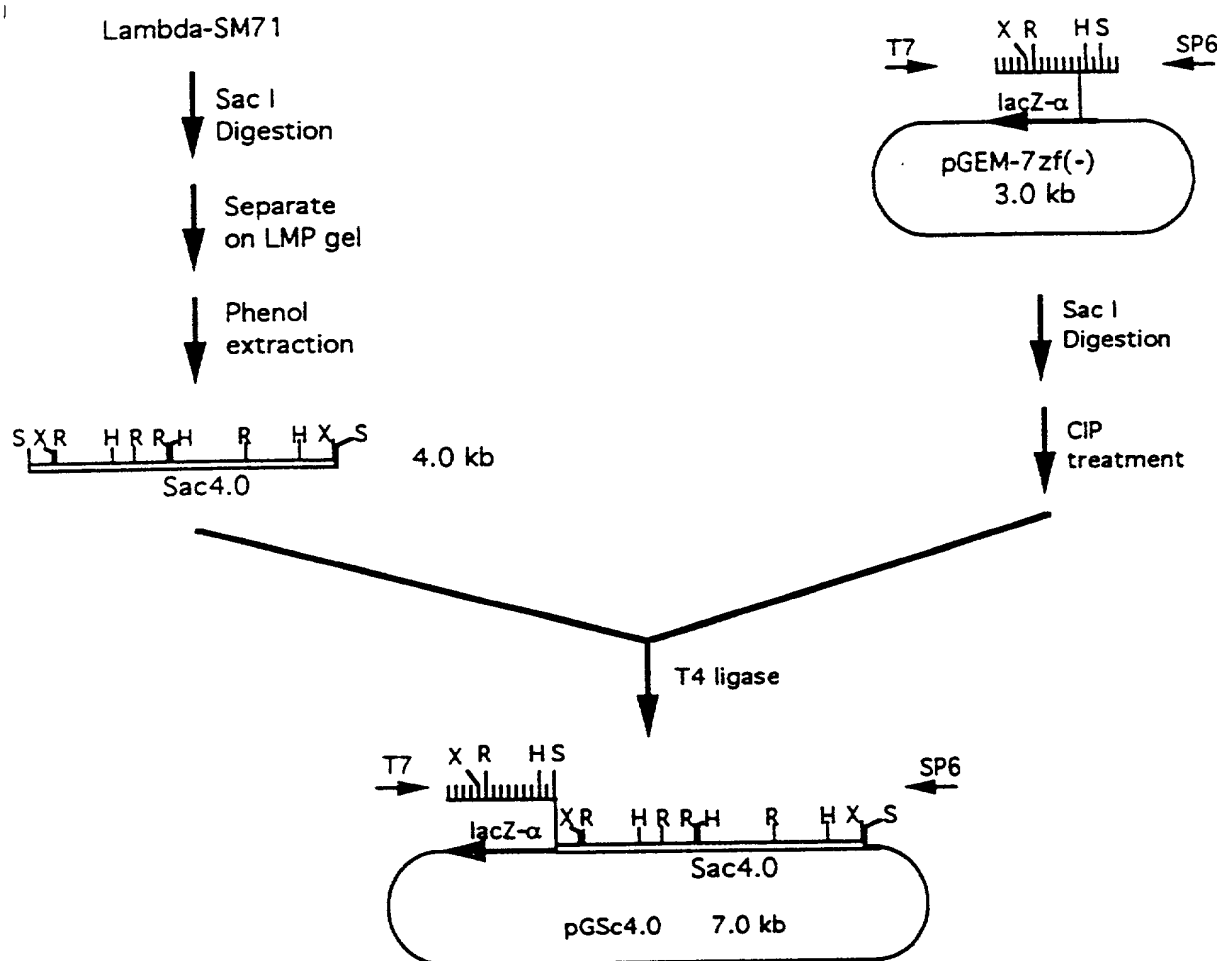
FIGURE 6

Map of Human *BCL-6* Locus



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FIGURE 7

pGSc4.0 Plasmid Construction



Lambda-SM71 = a recombinant Lambda phage clone  
containing *Bcl*-6 breakpoint

H = Hind III

R = EcoR I

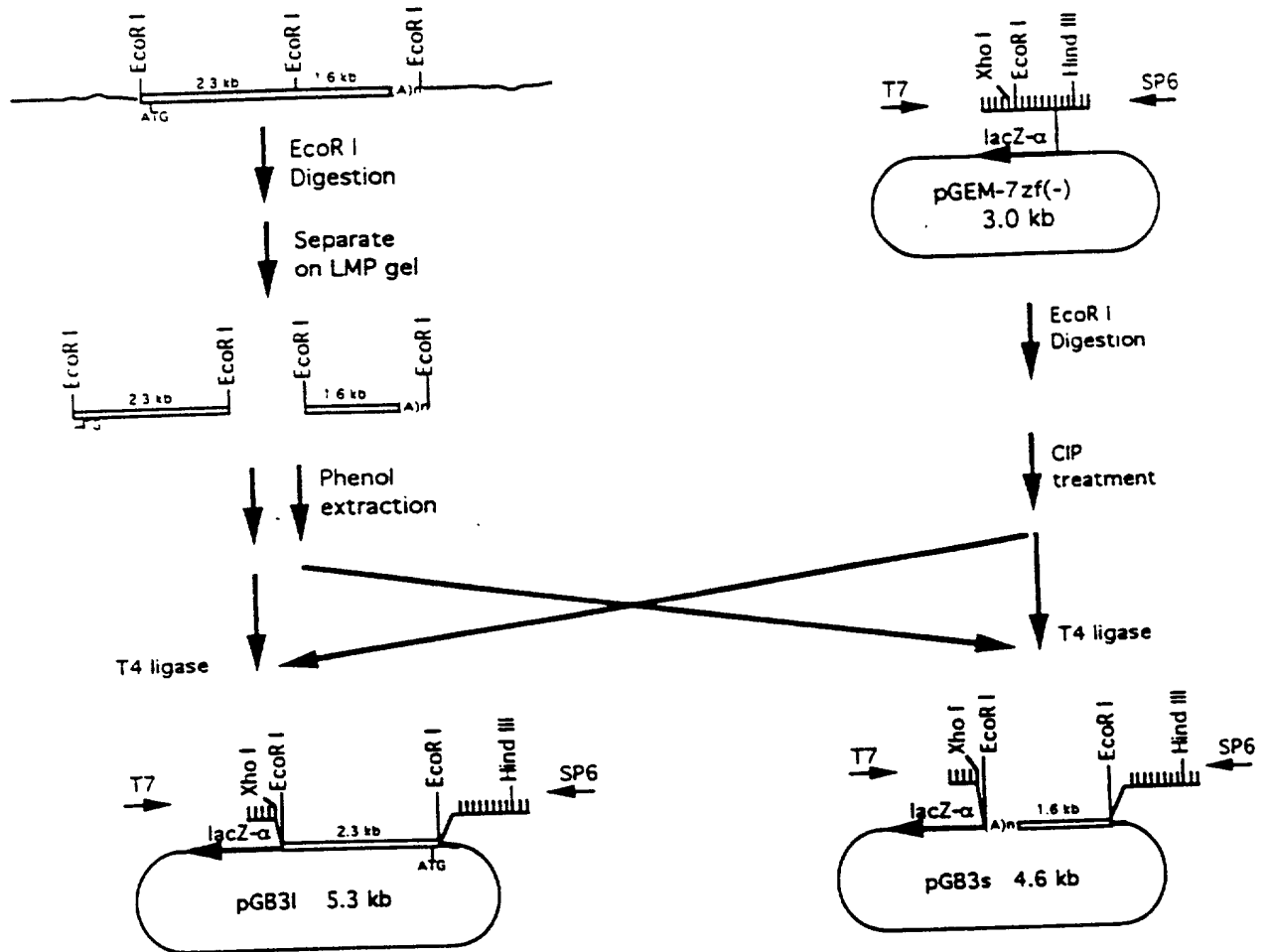
S = Sac I

X = Xho I

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FIGURE 8

pGb3I and pGB3s Plasmids Construction

Lambda-B31





## SEQ. ID. NOS. 1-2

## cdDNA and Amino Acid Sequences of BCL-6

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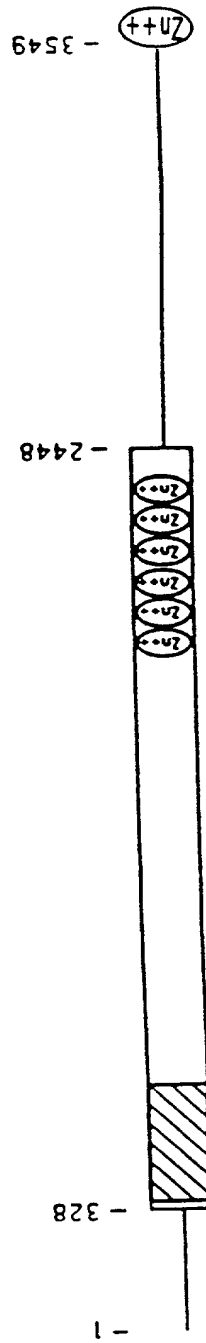
[illegible]

1

[illegible]

[illegible]

FIGURE 10A



## FIGURE 10B

1 MASPADSCIQ FTRHASDVLL NLNRLRSRDI LTDVVIVVSR EQFRAHKTVL  
 51 MACSGLFYSI FTDQLKCNLS VINLDPEINP EGFCILLDFM YTSRLNLREG  
 101 NIMAVMATAM YLQMEHVVDI CRKFIKASEA EMVSAIKPPR EEFLNSRMLM  
 151 PQDIMAYRGR EVVENNLPLR SAPGCESRAF APSLYSGLST PPASYSMYSH  
 201 LPVSSLLFSD EEFRDVRMPV ANPFPKERAL PCDSARVPG EYSRPTLEVS  
 251 PNVCHSNIYS PKETIPEEAR SDMHYSVAEG LKPAAPSARN APYFPCDKAS  
 301 KEEERPSSD EIALHFEPN APLNRKGLVS PQSPQKSDCQ PNSPTEACSS  
 351 KNACILQASG SPPAKSPTDP KACNWKKYKF IVLNSLNQNA KPGGPEQAEI  
 401 GRLSPRAYTA PPACQPPMEP ENLDLQSPK LSASGEDSTI PQASRLNNIV  
 451 NRSMTGSPRS SSESHPLYM HPPKCTSCGS QSPQHAEMCL HTAGPTFAEE  
 501 MGETQSEYSD SSCENGAFPC **NECDCRFSEE ASLKRHTLQT** HSDKPYK **CDR**  
 551 **CQASFRYKGN LASHKTVHTG** EKPYR **CNIG AQFNRPANLK THTRIHS** GEK  
 601 PYK **CETCGAR FVQVAHLRAH VLIHT** GEKPY **PCETCGTRFR HLOTLEKSHLR**  
 651 **IHT** GEKPYH **EKNLHFRHK SOLRLHLROK** HGAITNTKVQ YRVSATDLPP  
 701 ELPKAC

# FIGURE 11

ZFPJS (2-56)	D G S F V R L Q E E N K O R E K G Q Y C D A T L D V G G L V F K A H R A V L A C C S H F F Q S L Y G
KUP (1-54)	W D T A S H L V L Q Q N M O R E F G F L C D C T V A N G D V Y F K A H R A V L A C C S H F F Q S L Y G
VA55R (1-51)	M N N E L A V D N G F R N S G R F C D I S T A V A N G D V Y F K A H R A V L A C C S H F F Q S L Y G
tlk (9-83)	C K R W N H Q L N L L S V F D Q L L H A E T F T D V V E G G H L K A H K N V L S A C S P Y F N T L F V
Kelch (132-188)	Q Y S N E H H Y C L C K A N Q R L A G T L C D V I L V A D V E I H A H R M V L A S C S P Y F Y A M F T
PLZF (10-83)	Q K Q N P S H L C L L N L N R R S R D I L T D V V V M V D S D E F F H A H R T V L A C T S K M F E I L F
BCL-6 (8-62)	C K Q F T R H A A D M L L N L N R R S R D I L T D V V V M V D S D E F F H A H R T V L A C T S K M F E I L F
ZFPJS (57-104)	S G G S V L P A G F V E I P G L L L D F F Y T Q H L A L T S G N R D Q V L A A R E L L R V
KUP (55-107)	S S E C I K Q P P D I L Q L L S Y L L H I M Y T Q H L A L T S G N R D Q V L A A R E L L R V
VA55R (52-106)	N N F I D S N E Y E N L H Q L L S Y L L H I M Y T Q H L A L T S G N R D Q V L A A R E L L R V
tlk (84-116)	S H . . . E K H P I L L K D P P A R L L E L L L D F F Y T Q H L A L T S G N R D Q V L A A R E L L R V
Kelch (187-240)	S F E E S R Q A R I T L Q M . . . S P K F Q Q L L E L L L D F F Y T Q H L A L T S G N R D Q V L A A R E L L R V
PLZF (84-114)	. . . H R N S Q H Y T L D F . . . S P K F Q Q L L E L L L D F F Y T Q H L A L T S G N R D Q V L A A R E L L R V
BCL-6 (63-117)	D Q L K C N L S V I N L D E E N L A A F C I L L D F F Y T Q H L A L T S G N R D Q V L A A R E L L R V

FIGURE 12

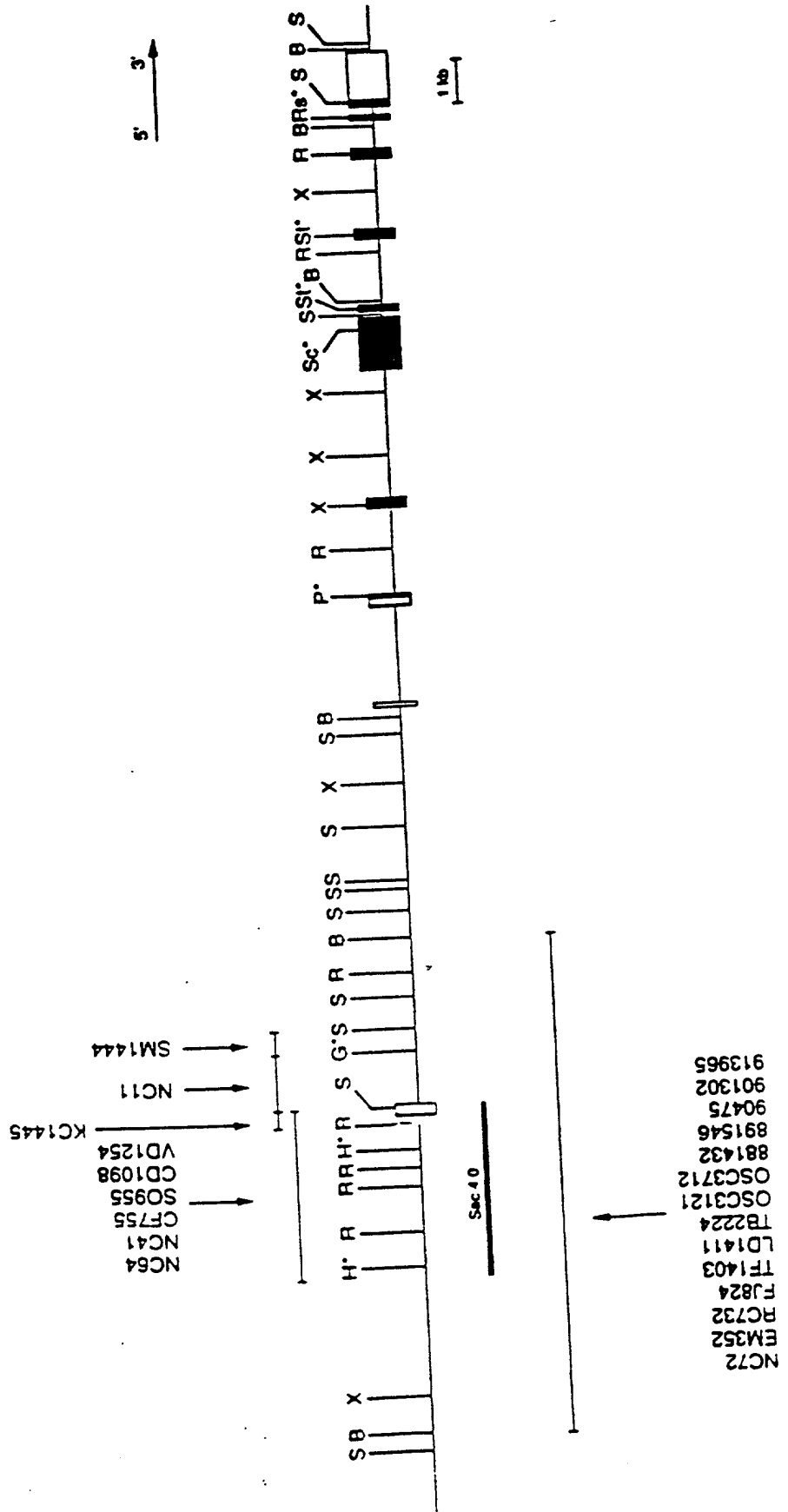




FIGURE 13A

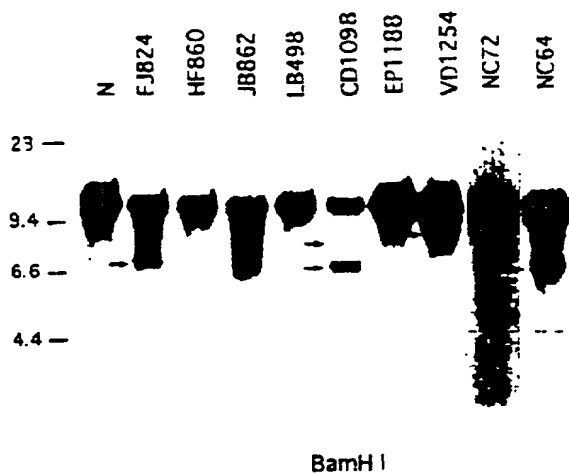


FIGURE 13B

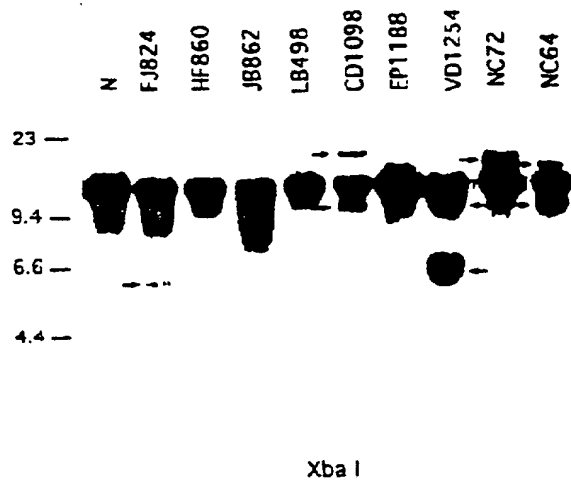


FIGURE 14C

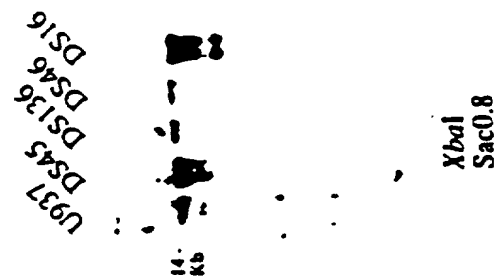


FIGURE 14B

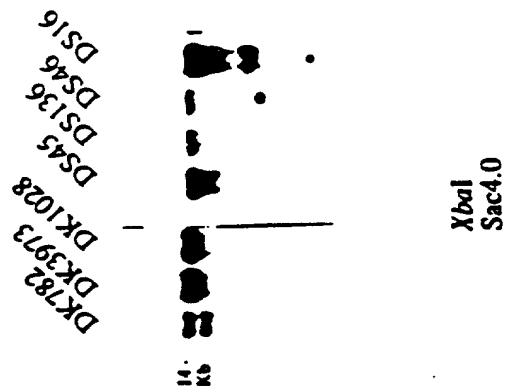
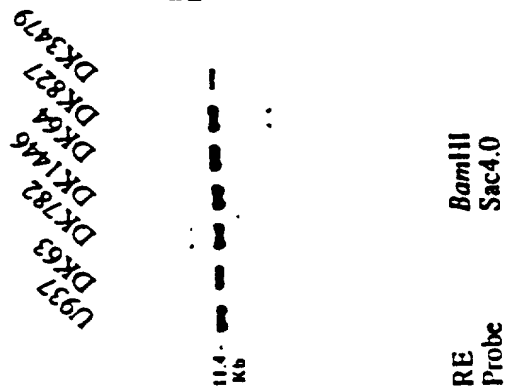


FIGURE 14A



DS16	→
DK827	→
DK771	→
DK1178	→
DK782	→

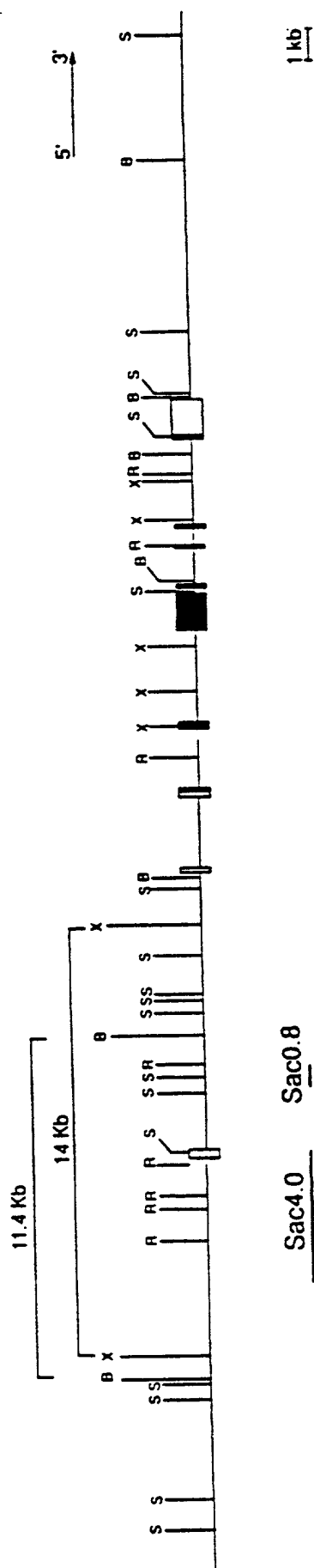


FIGURE 16A

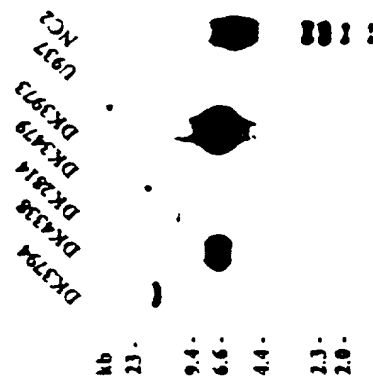


FIGURE 16B

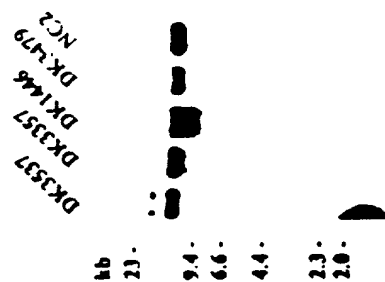


FIGURE 16C

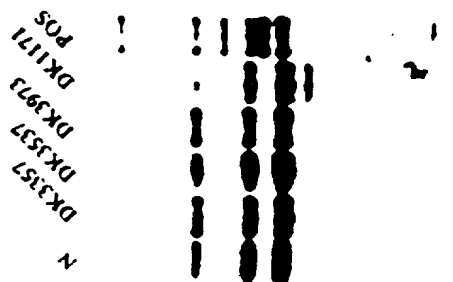


FIGURE 17A

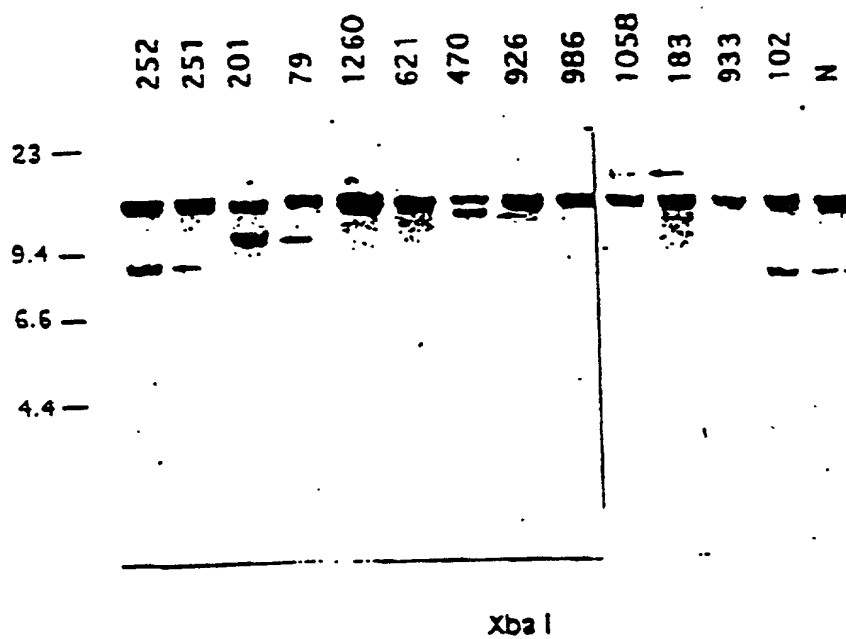


FIGURE 17B

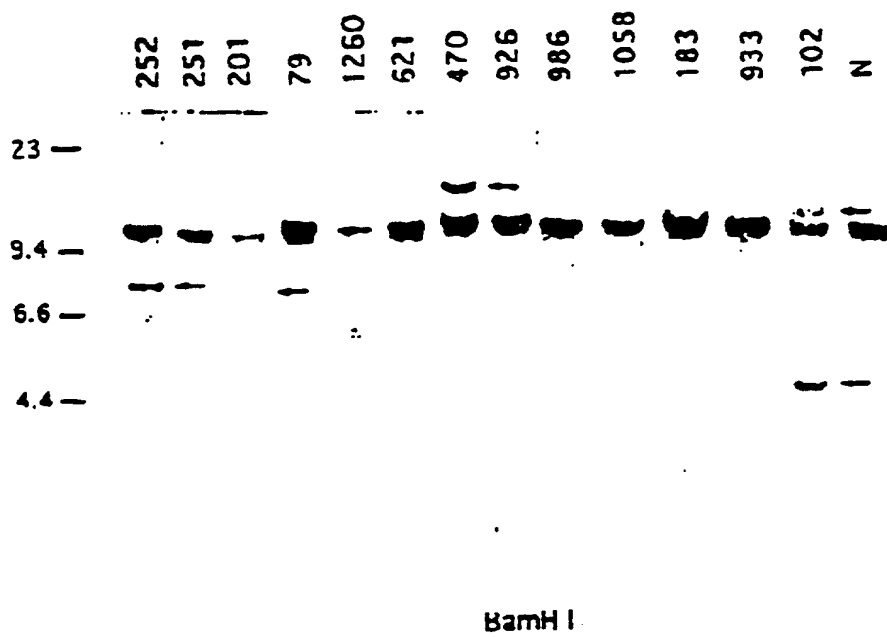


FIGURE 18A

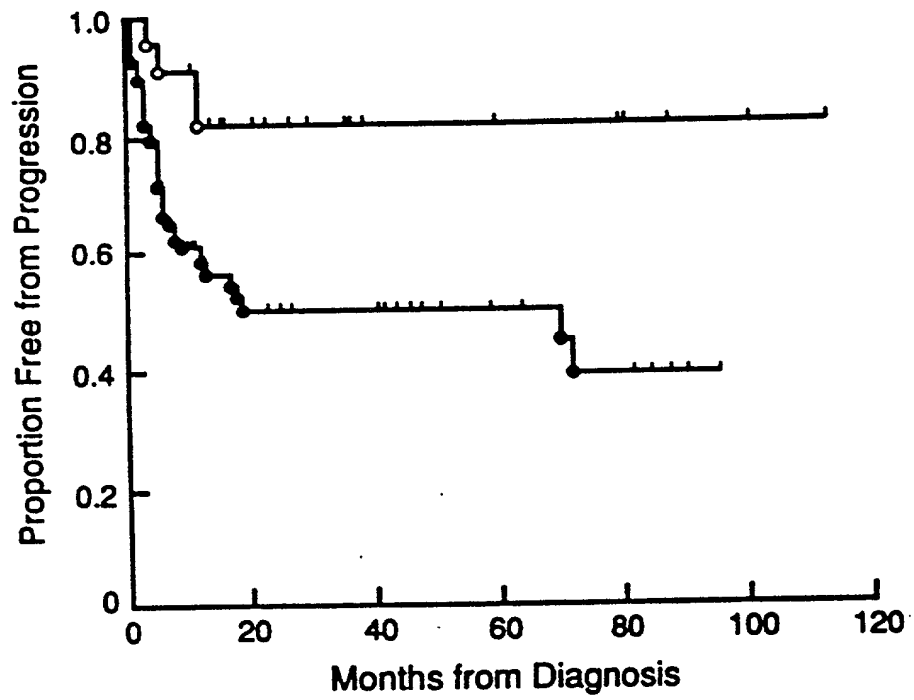


FIGURE 18B

